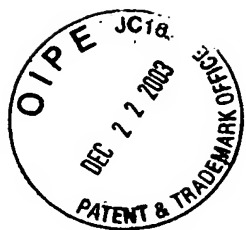


Replacement Sheet

**Figure 1A**

Identity to SeqID No:1 is indicated by a dot. Gap is indicated by a dash.

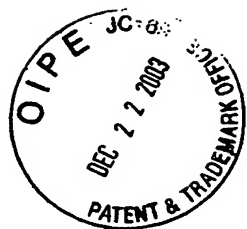
|        |                                  |     |     |
|--------|----------------------------------|-----|-----|
| *      | 20                               | *   |     |
| Seqid1 | : ATGTCTAAGCCTACTTTGATAAAAACAACC | :   | 30  |
| Seqid3 | : .....                          | :   | 30  |
|        | 40                               | *   | 60  |
| Seqid1 | : TTAATTTGTGCCTTAAGTGCATTGATGCTC | :   | 60  |
| Seqid3 | : .....                          | :   | 60  |
|        | *                                | 80  | *   |
| Seqid1 | : AGTGGTTGTAGCAATCAAGCGGACAAAGCC | :   | 90  |
| Seqid3 | : .....                          | :   | 90  |
|        | 100                              | *   | 120 |
| Seqid1 | : GCCCAGCCAAAAAGCAGCACGGTAGACGCT | :   | 120 |
| Seqid3 | : .....                          | :   | 120 |
|        | *                                | 140 | *   |
| Seqid1 | : GCCGCCAAGACAGCAAATGCAGATAATGCT | :   | 150 |
| Seqid3 | : .....                          | :   | 150 |
|        | 160                              | *   | 180 |
| Seqid1 | : GCCTCACAAGAACATCAAGGCGAGCTGCCT | :   | 180 |
| Seqid3 | : .....                          | :   | 180 |



Replacement Sheet

**Figure 1B**

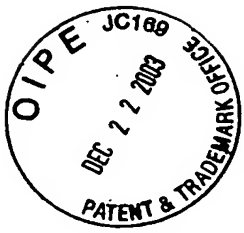
|        |   |                                |   |     |
|--------|---|--------------------------------|---|-----|
|        | * | 200                            | * |     |
| Seqid1 | : | GTCATTGATGCCATTGTTACGCATGCACCA | : | 210 |
| Seqid3 | : | .....                          | : | 210 |
|        |   | 220                            | * | 240 |
| Seqid1 | : | GAAGTTCCACCACCTGTTGACCGTGACCAC | : | 240 |
| Seqid3 | : | .....                          | : | 240 |
|        | * | 260                            | * |     |
| Seqid1 | : | CCCGCCAAAGTGGTGGTAAAAATGGAAACC | : | 270 |
| Seqid3 | : | .....                          | : | 270 |
|        |   | 280                            | * | 300 |
| Seqid1 | : | GTTGAAAAAGTCATGCGTCTGGCAGATGGC | : | 300 |
| Seqid3 | : | .....                          | : | 300 |
|        | * | 320                            | * |     |
| Seqid1 | : | GTGGAATATCAGTTTTGGACATTTGGCGGT | : | 330 |
| Seqid3 | : | .....                          | : | 330 |
|        |   | 340                            | * | 360 |
| Seqid1 | : | CAAGTTCCAGGGCAGATGATTCGTGTGCGT | : | 360 |
| Seqid3 | : | .....                          | : | 360 |
|        | * | 380                            | * |     |
| Seqid1 | : | GAAGGCGACACCATCGAAGTGCAGTTCTCA | : | 390 |
| Seqid3 | : | .....                          | : | 390 |



Replacement Sheet

**Figure 1C**

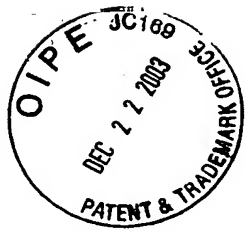
|        |     |                                |     |     |
|--------|-----|--------------------------------|-----|-----|
|        | 400 | *                              | 420 |     |
| Seqid1 | :   | AACCACCCAGATTCAAAAATGCCCCATAAT | :   | 420 |
| Seqid3 | :   | .....                          | :   | 420 |
|        |     |                                |     |     |
|        |     | *                              | 440 | *   |
| Seqid1 | :   | GTTGACTTTCACGCTGCCACAGGGCCTGGC | :   | 450 |
| Seqid3 | :   | .....                          | :   | 450 |
|        |     |                                |     |     |
|        | 460 | *                              | 480 |     |
| Seqid1 | :   | GGCGGGGCAGAAGCGTCATTACCGCACCG  | :   | 480 |
| Seqid3 | :   | .....                          | :   | 480 |
|        |     |                                |     |     |
|        |     | *                              | 500 | *   |
| Seqid1 | :   | GGTCATACATCAACCTTTAGTTTTAAAGCC | :   | 510 |
| Seqid3 | :   | .....                          | :   | 510 |
|        |     |                                |     |     |
|        | 520 | *                              | 540 |     |
| Seqid1 | :   | TTACAGCCTGGTTTGTATGTCTATCACTGT | :   | 540 |
| Seqid3 | :   | .....                          | :   | 540 |
|        |     |                                |     |     |
|        |     | *                              | 560 | *   |
| Seqid1 | :   | GCGGTTGCCCCTGTTGGCATGCACATTGCT | :   | 570 |
| Seqid3 | :   | .....                          | :   | 570 |
|        |     |                                |     |     |
|        | 580 | *                              | 600 |     |
| Seqid1 | :   | AATGGCATGTATGGTTTGATTTTGGTTGAA | :   | 600 |
| Seqid3 | :   | .....                          | :   | 600 |



Replacement Sheet

**Figure 1D**

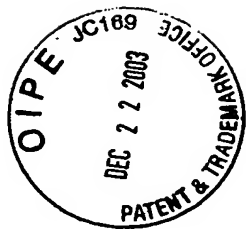
|        |   |                                 |       |
|--------|---|---------------------------------|-------|
|        | * | 620                             | *     |
| Seqid1 | : | CCAAAAGAGGGCTTGCCAAAAGTAGATAAA  | : 630 |
| Seqid3 | : | .....                           | : 630 |
|        |   |                                 |       |
|        |   | 640                             | * 660 |
| Seqid1 | : | GAATACTATGTCATGCAAGGCGACTTTTAT  | : 660 |
| Seqid3 | : | .....                           | : 660 |
|        |   |                                 |       |
|        | * | 680                             | *     |
| Seqid1 | : | ACCAAAGGCAAATATGGCGAACAAGGTCTA  | : 690 |
| Seqid3 | : | .....                           | : 690 |
|        |   |                                 |       |
|        |   | 700                             | * 720 |
| Seqid1 | : | CAGCCCTTTGATATGGAAAAAGCCATTCGA  | : 720 |
| Seqid3 | : | .....                           | : 720 |
|        |   |                                 |       |
|        | * | 740                             | *     |
| Seqid1 | : | GAAGATGCTGAATATGTTGTCTTTAATGGT  | : 750 |
| Seqid3 | : | .....                           | : 750 |
|        |   |                                 |       |
|        |   | 760                             | * 780 |
| Seqid1 | : | TCGGTGGGGGCGTTGACTGGTGAAAATGCT  | : 780 |
| Seqid3 | : | .....                           | : 780 |
|        |   |                                 |       |
|        | * | 800                             | *     |
| Seqid1 | : | CTAAAAGCCAAGGTTGGCGAAACTGTTTCGC | : 810 |
| Seqid3 | : | .....                           | : 810 |



Replacement Sheet

**Figure 1E**

|        |      |                                |      |      |
|--------|------|--------------------------------|------|------|
|        | 820  | *                              | 840  |      |
| Seqid1 | :    | TTATTTGTGGGTAACGGCGGCCCGAATTTG | :    | 840  |
| Seqid3 | :    | .....                          | :    | 840  |
|        |      |                                |      |      |
|        |      | *                              | 860  | *    |
| Seqid1 | :    | ACATCATCATTCATGTCATTGGTGAGATT  | :    | 870  |
| Seqid3 | :    | .....                          | :    | 870  |
|        |      |                                |      |      |
|        | 880  | *                              | 900  |      |
| Seqid1 | :    | TTTGATAAGGTTCACTTTGAGGGTGGTAAG | :    | 900  |
| Seqid3 | :    | .....                          | :    | 900  |
|        |      |                                |      |      |
|        |      | *                              | 920  | *    |
| Seqid1 | :    | GGTGAAAACCACAATATCCAAACCACGCTA | :    | 930  |
| Seqid3 | :    | .....                          | :    | 930  |
|        |      |                                |      |      |
|        | 940  | *                              | 960  |      |
| Seqid1 | :    | ATCCCAGCAGGTGGCGCTGCCATCACTGAA | :    | 960  |
| Seqid3 | :    | .....                          | :    | 960  |
|        |      |                                |      |      |
|        |      | *                              | 980  | *    |
| Seqid1 | :    | TTTAAGGTGGATGTGCCGGGTGATTATGTC | :    | 990  |
| Seqid3 | :    | .....                          | :    | 990  |
|        |      |                                |      |      |
|        | 1000 | *                              | 1020 |      |
| Seqid1 | :    | TTGGTTGACCATGCCATCTTCCGTGCCTTT | :    | 1020 |
| Seqid3 | :    | .....                          | :    | 1020 |



Replacement Sheet

**Figure 1F**

\*                      1040                      \*

Seqid1 : AACAAAGGGGCATTGGGCATACTTAAGGTG : 1050

Seqid3 : ..... : 1050

1060                      \*                      1080

Seqid1 : GAAGGTGAAGAAAATCATGAGATTTATTCA : 1080

Seqid3 : ..... : 1080

\*                      1100                      \*

Seqid1 : CACAAACAAACAGACGCTGTCTATCTGCCA : 1110

Seqid3 : ..... : 1110

1120                      \*                      1140

Seqid1 : GAGGGTGCCCCACAAGCAATTGATACCCAA : 1140

Seqid3 : ..... : 1140

\*                      1160                      \*

Seqid1 : GAAGCACCCAAAACACCTGCACCTGCCAAC : 1170

Seqid3 : ..... : 1170

1180                      \*                      1200

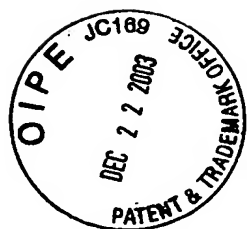
Seqid1 : TTACAAGAGCAGATTAAAGCAGGTAAGGCA : 1200

Seqid3 : ..... : 1200

\*                      1220                      \*

Seqid1 : ACCTATGACTCTAACTGTGCTGCTTGTCAC : 1230

Seqid3 : ..... : 1230



Replacement Sheet

**Figure 1G**

1240 \* 1260  
Seqid1 : CAACCTGATGGTAAAGGCGTGCCAAACGCT : 1260  
Seqid3 : ..... : 1260

\* 1280 \*  
Seqid1 : TTCCCACCGCTTGCCAACTCTGACTATCTG : 1290  
Seqid3 : ..... : 1290

1300 \* 1320  
Seqid1 : AACGCCGACCACGCTCGTGCCGCCAGCATC : 1320  
Seqid3 : ..... : 1320

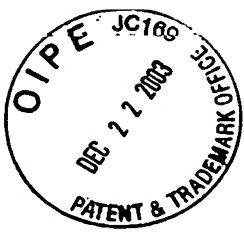
\* 1340 \*  
Seqid1 : GTGGCAAATGGATTGTCTGGTAAGATTACC : 1350  
Seqid3 : ..... : 1350

1360 \* 1380  
Seqid1 : GTCAATGGCAACCAATATGAAAGCGTCATG : 1380  
Seqid3 : ..... : 1380

\* 1400 \*  
Seqid1 : CCTGCGATTGCTCTGAGCGACCAACAGATT : 1410  
Seqid3 : ..... : 1410

```
Seqid1 : CCAAAGTGA : 1509
Seqid3 : .....--- : 1506
```





Replacement Sheet

**Figure 2A**

Identity to SeqID No:2 is indicated by a dot. Gap is indicated by a dash.

Seqid2 : MSKPTLIKTTLICALSALMLSGCSNQADKA : 30

Seqid4 : ..... : 30

40 \* 60

Seqid2 : AQPKSSTVDAAAKTANADNAASQEHQGELP : 60

Seqid4 : ..... : 60

\* 80 \*

Seqid2 : VIDAIVTHAPEVPPPVD RDHPAKVVVKMET : 90

Seqid4 : ..... : 90

100 \* 120

Seqid2 : VEKVMRLADGVEYQFWTFGGQVPGQMIRVR : 120

Seqid4 : ..... : 120

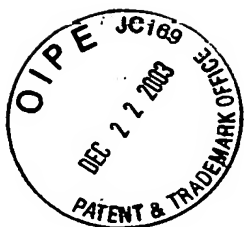
\* 140 \*

Seqid2 : EGDTIEVQFSNHPDSKMPHNVDFAATGPG : 150

Seqid4 : ..... : 150

160 \* 180

Seqid2 : GGAEASFTAPGHTSTFSFKALQPGLYVYHC : 180



Replacement Sheet

**Figure 2B**

Seqid4 : ..... : 180

\* 200 \*

Seqid2 : AVAPVGMHIANGMYGLILVEPK EGLPKVDK : 210

Seqid4 : ..... : 210

220 \* 240

Seqid2 : EYYVMQGDFYTKGKYGEQGLQPFDMEKAIR : 240

Seqid4 : ..... : 240

\* 260 \*

Seqid2 : EDAEYVVFNGSVGALTGENALKAKVGETVR : 270

Seqid4 : ..... : 270

280 \* 300

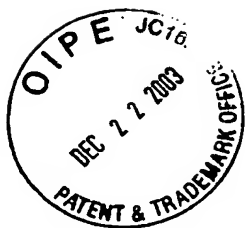
Seqid2 : LFVGNGGPNLTSSFHVIGEIFDKVHFEGGK : 300

Seqid4 : ..... : 300

\* 320 \*

Seqid2 : GENHNIQTTLIPAGGAAITEFKVDVPGDYV : 330

Seqid4 : ..... : 330



Replacement Sheet

**Figure 2C**

340 \* 360  
Seqid2 : LVDHAI FRAFNKGALGILKVEGEENHEIYS : 360  
Seqid4 : ..... : 360

\* 380 \*  
Seqid2 : HKQTD AVYLPEGAPQAIDTQEAPKTPAPAN : 390  
Seqid4 : ..... : 390

400 \* 420  
Seqid2 : LQE QIKAGKATYDSNCAACHQPDGKGV PNA : 420  
Seqid4 : ..... : 420

\* 440 \*  
Seqid2 : FPPLANS DYLNADHARAASIVANGLSGKIT : 450  
Seqid4 : ..... : 450

460 \* 480  
Seqid2 : VNGNQYESVMPAIALSDQQIANVITYTLNS : 480  
Seqid4 : ..... : 480



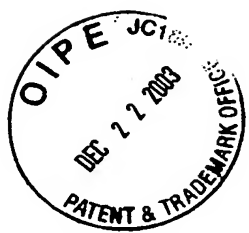
Replacement Sheet

**Figure 2D**

\* 500

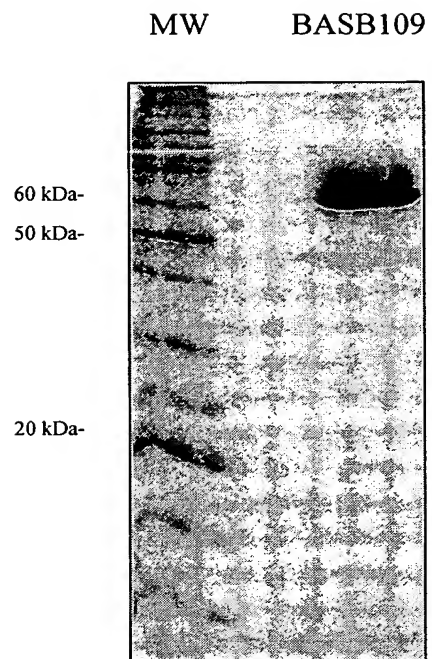
Seqid2 : FG NKGGQLSADDVAKAKKTKPN : 502

Seqid4 : ..... : 502



Replacement Sheet

**Figure 3-A**



**Fig. 3-B**

